RAW SEQUENCE LISTING DATE: 06/06/2003
PATENT APPLICATION: **US/10/045,400C** TIME: 08:03:09

Input Set : **A:\P-CAN 1004 Sequence Listing.txt**
Output Set: **N:\CRF4\06062003\J045400C.raw**

```
      3 <110> APPLICANT: Moon, Chulso
      4       Mao, Li
      6 <120> TITLE OF INVENTION: DAP-Kinase and HOXA9, Two Human Genes Associated with
Genesis,
      7       Progression, and Aggressiveness of Non-Small Cell Lung Cancer
      9 <130> FILE REFERENCE: 10620-1U1
     11 <140> CURRENT APPLICATION NUMBER: 10/045,400C
     12 <141> CURRENT FILING DATE: 2001-11-29
     14 <150> PRIOR APPLICATION NUMBER: US 60/250,083
     15 <151> PRIOR FILING DATE: 2000-11-29
     17 <160> NUMBER OF SEQ ID NOS: 7
     19 <170> SOFTWARE: PatentIn version 3.1
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 20
     23 <212> TYPE: DNA
     24 <213> ORGANISM: Artificial
     26 <220> FEATURE:
     27 <223> OTHER INFORMATION: HoxA9 PCR Primer
     29 <400> SEQUENCE: 1
     30 ccggccttat ggcattaaac                                              20
     33 <210> SEQ ID NO: 2
     34 <211> LENGTH: 20
     35 <212> TYPE: DNA
     36 <213> ORGANISM: Artificial
     38 <220> FEATURE:
     39 <223> OTHER INFORMATION: HoxA9 PCR Primer
     41 <400> SEQUENCE: 2
     42 agttggctgc tgggttattg                                              20
     45 <210> SEQ ID NO: 3
     46 <211> LENGTH: 218
     47 <212> TYPE: DNA
     48 <213> ORGANISM: Artificial
     50 <220> FEATURE:
     51 <223> OTHER INFORMATION: HoxA9 Probe
     53 <400> SEQUENCE: 3
     54 ccggccttat ggcattaaac ctgaaccgct gtcggccaga aggggtgact gtcccacgct     60
     56 tgacactcac actttgtccc tgactgacta tgcttgtggt tctcctccag ttgatagaga    120
     58 aaaacaaccc agcgaaggcg ccttctccga aaacaatgcc gagaatgaga gcggcggaga    180
     60 caagcccccc atcgatccca ataacccagc agccaact                           218
     63 <210> SEQ ID NO: 4
     64 <211> LENGTH: 5910
     65 <212> TYPE: DNA
     66 <213> ORGANISM: Homo sapiens
     68 <220> FEATURE:
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     69 <221> NAME/KEY: CDS
     70 <222> LOCATION: (337)..(4632)
     71 <223> OTHER INFORMATION:
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     74 cggaggacag ccggaccgag ccaacgccgg ggactttgtt ccctccacgg aggggactcg      60
     76 gcaactcgca gcggcagggt ctggggccgg cgcctgggag ggatctgcgc cccccactca     120
     78 ctccctagct gtgttcccgc cgccgccccg gctagtctcc ggcgctggcg cctatggtcg     180
     80 gcctccgaca gcgctccgga gggaccgggg gagctcccag gcgcccggga ctggagactg     240
     82 atgcatgagg ggcctacgga ggcgcaggag cggtggtgat ggtctgggaa gcggagctga     300
     84 agtcccctgg gctttggtga ggcgtgacag tttatc atg acc gtg ttc agg cag      354
     85                                       Met Thr Val Phe Arg Gln
     86                                       1               5
     88 gaa aac gtg gat gat tac tac gac acc ggc gag gaa ctt ggc agt gga      402
     89 Glu Asn Val Asp Asp Tyr Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly
     90             10                  15                  20
     92 cag ttt gcg gtt gtg aag aaa tgc cgt gag aaa agt acc ggc ctc cag      450
     93 Gln Phe Ala Val Val Lys Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln
     94         25                  30                  35
     96 tat gcc gcc aaa ttc atc aag aaa agg agg act aag tcc agc cgg cgg      498
     97 Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg
     98     40                  45                  50
    100 ggt gtg agc cgc gag gac atc gag cgg gag gtc agc atc ctg aag gag      546
    101 Gly Val Ser Arg Glu Asp Ile Glu Arg Glu Val Ser Ile Leu Lys Glu
    102 55                  60                  65                  70
    104 atc cag cac ccc aat gtc atc acc ctg cac gag gtc tat gag aac aag      594
    105 Ile Gln His Pro Asn Val Ile Thr Leu His Glu Val Tyr Glu Asn Lys
    106                 75                  80                  85
    108 acg gac gtc atc ctg atc ttg gaa ctc gtt gca ggt ggc gag ctg ttt      642
    109 Thr Asp Val Ile Leu Ile Leu Glu Leu Val Ala Gly Gly Glu Leu Phe
    110             90                  95                  100
    112 gac ttc tta gct gaa aag gaa tct tta act gaa gag gaa gca act gaa      690
    113 Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr Glu Glu Glu Ala Thr Glu
    114         105                 110                 115
    116 ttt ctc aaa caa att ctt aat ggt gtt tac tac ctg cac tcc ctt caa      738
    117 Phe Leu Lys Gln Ile Leu Asn Gly Val Tyr Tyr Leu His Ser Leu Gln
    118     120                 125                 130
    120 atc gcc cac ttt gat ctt aag cct gag aac ata atg ctt ttg gat aga      786
    121 Ile Ala His Phe Asp Leu Lys Pro Glu Asn Ile Met Leu Leu Asp Arg
    122 135                 140                 145                 150
    124 aat gtc ccc aaa cct cgg atc aag atc att gac ttt ggg ttg gcc cat      834
    125 Asn Val Pro Lys Pro Arg Ile Lys Ile Ile Asp Phe Gly Leu Ala His
    126                 155                 160                 165
    128 aaa att gac ttt gga aat gaa ttt aaa aac ata ttt ggg act cca gag      882
    129 Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu
    130             170                 175                 180
    132 ttt gtc gct cct gag ata gtc aac tat gaa cct ctt ggt ctt gag gca      930
    133 Phe Val Ala Pro Glu Ile Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala
    134         185                 190                 195
    136 gat atg tgg agt atc ggg gta ata acc tat atc ctc cta agt ggg gcc      978
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```
137 Asp Met Trp Ser Ile Gly Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala
138     200                 205                 210
140 tcc cca ttt ctt gga gac act aag caa gaa acg tta gca aat gta tcc     1026
141 Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Val Ser
142 215                 220                 225                 230
144 gct gtc aac tac gaa ttt gag gat gaa tac ttc agt aat acc agt gcc     1074
145 Ala Val Asn Tyr Glu Phe Glu Asp Glu Tyr Phe Ser Asn Thr Ser Ala
146                 235                 240                 245
148 cta gcc aaa gat ttc ata aga aga ctt ctg gtc aag gat cca aag aag     1122
149 Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu Val Lys Asp Pro Lys Lys
150             250                 255                 260
152 aga atg aca att caa gat agt ttg cag cat ccc tgg atc aag cct aaa     1170
153 Arg Met Thr Ile Gln Asp Ser Leu Gln His Pro Trp Ile Lys Pro Lys
154         265                 270                 275
156 gat aca caa cag gca ctt agt aga aaa gca tca gca gta aac atg gag     1218
157 Asp Thr Gln Gln Ala Leu Ser Arg Lys Ala Ser Ala Val Asn Met Glu
158     280                 285                 290
160 aaa ttc aag aag ttt gca gcc cgg aaa aaa tgg aaa caa tcc gtt cgc     1266
161 Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys Trp Lys Gln Ser Val Arg
162 295                 300                 305                 310
164 ttg ata tca ctg tgc caa aga tta tcc agg tca ttc ctg tcc aga agt     1314
165 Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg Ser Phe Leu Ser Arg Ser
166                 315                 320                 325
168 aac atg agt gtt gcc aga agc gat gat act ctg gat gag gaa gac tcc     1362
169 Asn Met Ser Val Ala Arg Ser Asp Asp Thr Leu Asp Glu Glu Asp Ser
170             330                 335                 340
172 ttt gtg atg aaa gcc atc atc cat gcc atc aac gat gac aat gtc cca     1410
173 Phe Val Met Lys Ala Ile Ile His Ala Ile Asn Asp Asp Asn Val Pro
174         345                 350                 355
176 ggc ctg cag cac ctt ctg ggc tca tta tcc aac tat gat gtt aac caa     1458
177 Gly Leu Gln His Leu Leu Gly Ser Leu Ser Asn Tyr Asp Val Asn Gln
178     360                 365                 370
180 ccc aac aag cac ggg aca cct cca tta ctc att gct gct ggc tgt ggg     1506
181 Pro Asn Lys His Gly Thr Pro Pro Leu Leu Ile Ala Ala Gly Cys Gly
182 375                 380                 385                 390
184 aat att caa ata cta cag ttg ctc att aaa aga ggc tcg aga atc gat     1554
185 Asn Ile Gln Ile Leu Gln Leu Leu Ile Lys Arg Gly Ser Arg Ile Asp
186                 395                 400                 405
188 gtc cag gat aag ggc ggg tcc aat gcc gtc tac tgg gct gct cgg cat     1602
189 Val Gln Asp Lys Gly Gly Ser Asn Ala Val Tyr Trp Ala Ala Arg His
190             410                 415                 420
192 ggc cac gtc gat acc ttg aaa ttt ctc agt gag aac aaa tgc cct ttg     1650
193 Gly His Val Asp Thr Leu Lys Phe Leu Ser Glu Asn Lys Cys Pro Leu
194         425                 430                 435
196 gat gtg aaa gac aag tct gga gag atg gcc ctc cac gtg gca gct cgc     1698
197 Asp Val Lys Asp Lys Ser Gly Glu Met Ala Leu His Val Ala Ala Arg
198     440                 445                 450
200 tat ggc cat gct gac gtg gct caa gtt act tgt gca gct tcg gct caa     1746
201 Tyr Gly His Ala Asp Val Ala Gln Val Thr Cys Ala Ala Ser Ala Gln
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202 455                 460                 465                 470
204 atc cca ata tcc agg aca aag gaa gaa gaa acc ccc ctg cac tgt gct     1794
205 Ile Pro Ile Ser Arg Thr Lys Glu Glu Glu Thr Pro Leu His Cys Ala
206                 475                 480                 485
208 gct tgg cac ggc tat tac tct gtg gcc aaa gcc ctt tgt gaa gcc ggc     1842
209 Ala Trp His Gly Tyr Tyr Ser Val Ala Lys Ala Leu Cys Glu Ala Gly
210             490                 495                 500
212 tgt aac gtg aac atc aag aac cga gaa gga gag acg ccc ctc ctg aca     1890
213 Cys Asn Val Asn Ile Lys Asn Arg Glu Gly Glu Thr Pro Leu Leu Thr
214         505                 510                 515
216 gcc tct gcc agg ggc tac cac gac atc gtg gag tgt ctg gcc gaa cat     1938
217 Ala Ser Ala Arg Gly Tyr His Asp Ile Val Glu Cys Leu Ala Glu His
218     520                 525                 530
220 gga gcc gac ctt aat gct tgc gac aag gac gga cac att gcc ctt cat     1986
221 Gly Ala Asp Leu Asn Ala Cys Asp Lys Asp Gly His Ile Ala Leu His
222 535                 540                 545                 550
224 ctg gct gta aga cgg tgt cag atg gag gta atc aag act ctc ctc agc     2034
225 Leu Ala Val Arg Arg Cys Gln Met Glu Val Ile Lys Thr Leu Leu Ser
226                 555                 560                 565
228 caa ggg tgt ttc gtc gat tat caa gac agg cac ggc aat act ccc ctc     2082
229 Gln Gly Cys Phe Val Asp Tyr Gln Asp Arg His Gly Asn Thr Pro Leu
230             570                 575                 580
232 cat gtg gca tgt aaa gat ggc aac atg cct atc gtg gtg gcc ctc tgt     2130
233 His Val Ala Cys Lys Asp Gly Asn Met Pro Ile Val Val Ala Leu Cys
234         585                 590                 595
236 gaa gca aac tgc aat ttg gac atc tcc aac aag tat ggg cga acg cct     2178
237 Glu Ala Asn Cys Asn Leu Asp Ile Ser Asn Lys Tyr Gly Arg Thr Pro
238     600                 605                 610
240 ctg cac ctt gcg gcc aac aac gga atc cta gac gtg gtc cgg tat ctc     2226
241 Leu His Leu Ala Ala Asn Asn Gly Ile Leu Asp Val Val Arg Tyr Leu
242 615                 620                 625                 630
244 tgt ctg atg gga gcc agc gtt gag gcg ctg acc acg gac gga aag acg     2274
245 Cys Leu Met Gly Ala Ser Val Glu Ala Leu Thr Thr Asp Gly Lys Thr
246                 635                 640                 645
248 gca gaa gat ctt gct aga tcg gaa cag cac gag cac gta gca ggt ctc     2322
249 Ala Glu Asp Leu Ala Arg Ser Glu Gln His Glu His Val Ala Gly Leu
250             650                 655                 660
252 ctt gca aga ctt cga aag gat acg cac cga gga ctc ttc atc cag cag     2370
253 Leu Ala Arg Leu Arg Lys Asp Thr His Arg Gly Leu Phe Ile Gln Gln
254         665                 670                 675
256 ctc cga ccc aca cag aac ctg cag cca aga att aag ctc aag ctg ttt     2418
257 Leu Arg Pro Thr Gln Asn Leu Gln Pro Arg Ile Lys Leu Lys Leu Phe
258     680                 685                 690
260 ggc cac tcg gga tcc ggg aaa acc acc ctt gta gaa tct ctc aag tgt     2466
261 Gly His Ser Gly Ser Gly Lys Thr Thr Leu Val Glu Ser Leu Lys Cys
262 695                 700                 705                 710
264 ggg ctg ctg agg agc ttt ttc aga agg cgt cgg ccc aga ctg tct tcc     2514
265 Gly Leu Leu Arg Ser Phe Phe Arg Arg Arg Arg Pro Arg Leu Ser Ser
266                 715                 720                 725
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Input Set : A:\P-CAN 1004 Sequence Listing.txt
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268 acc aac tcc agc agg ttc cca cct tca ccc ctg gct tct aag ccc aca     2562
269 Thr Asn Ser Ser Arg Phe Pro Pro Ser Pro Leu Ala Ser Lys Pro Thr
270             730                 735                 740
272 gtc tca gtg agc atc aac aac ctg tac cca ggc tgc gag aac gtg agt     2610
273 Val Ser Val Ser Ile Asn Asn Leu Tyr Pro Gly Cys Glu Asn Val Ser
274         745                 750                 755
276 gtg agg agc cgc agc atg atg ttc gag ccg ggt ctt acc aaa ggg atg     2658
277 Val Arg Ser Arg Ser Met Met Phe Glu Pro Gly Leu Thr Lys Gly Met
278     760                 765                 770
280 ctg gag gtg ttt gtg gcc ccg acc cac cac ccg cac tgc tcg gcc gat     2706
281 Leu Glu Val Phe Val Ala Pro Thr His His Pro His Cys Ser Ala Asp
282 775                 780                 785                 790
284 gac cag tcc acc aag gcc atc gac atc cag aac gct tat ttg aat gga     2754
285 Asp Gln Ser Thr Lys Ala Ile Asp Ile Gln Asn Ala Tyr Leu Asn Gly
286                 795                 800                 805
288 gtt ggc gat ttc agc gtg tgg gag ttc tct gga aat cct gtg tat ttc     2802
289 Val Gly Asp Phe Ser Val Trp Glu Phe Ser Gly Asn Pro Val Tyr Phe
290             810                 815                 820
292 tgc tgt tat gac tat ttt gct gca aat gat ccc acg tca atc cat gtt     2850
293 Cys Cys Tyr Asp Tyr Phe Ala Ala Asn Asp Pro Thr Ser Ile His Val
294         825                 830                 835
296 gtt gtc ttt agt ctá gaa gag ccc tat gag atc cag ctg aac cca gtg     2898
297 Val Val Phe Ser Leu Glu Glu Pro Tyr Glu Ile Gln Leu Asn Pro Val
298     840                 845                 850
300 att ttc tgg ctc agt ttc ctg aag tcc ctt gtc cca gtt gaa gaa ccc     2946
301 Ile Phe Trp Leu Ser Phe Leu Lys Ser Leu Val Pro Val Glu Glu Pro
302 855                 860                 865                 870
304 ata gcc ttc ggt ggc aag ctg aag aac cca ctc caa gtt gtc ctg gtg     2994
305 Ile Ala Phe Gly Gly Lys Leu Lys Asn Pro Leu Gln Val Val Leu Val
306                 875                 880                 885
308 gcc acc cac gct gac atc atg aat gtt cct cga ccg gct gga ggc gag     3042
309 Ala Thr His Ala Asp Ile Met Asn Val Pro Arg Pro Ala Gly Gly Glu
310             890                 895                 900
312 ttt gga tat gac aaa gac aca tcg ttg ctg aaa gag att agg aac agg     3090
313 Phe Gly Tyr Asp Lys Asp Thr Ser Leu Leu Lys Glu Ile Arg Asn Arg
314         905                 910                 915
316 ttt gga aat gat ctt cac att tca aat aag ctg ttt gtt ctg gat gct     3138
317 Phe Gly Asn Asp Leu His Ile Ser Asn Lys Leu Phe Val Leu Asp Ala
318     920                 925                 930
320 ggg gct tct ggg tca aag gac atg aag gta ctt cga aat cat ctg caa     3186
321 Gly Ala Ser Gly Ser Lys Asp Met Lys Val Leu Arg Asn His Leu Gln
322 935                 940                 945                 950
324 gaa ata cga agc cag att gtt tcg gtc tgt cct ccc atg act cac ctg     3234
325 Glu Ile Arg Ser Gln Ile Val Ser Val Cys Pro Pro Met Thr His Leu
326                 955                 960                 965
328 tgt gag aaa atc atc tcc acg ctg cct tcc tgg agg aag ctc aat gga     3282
329 Cys Glu Lys Ile Ile Ser Thr Leu Pro Ser Trp Arg Lys Leu Asn Gly
330             970                 975                 980
332 ccc aac cag ctg atg tcg ctg cag cag ttt gtg tac gac gtg cag gac     3330
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L:73 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71
L:882 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:880